

# SCORE Search Results Details for Application 10552515 and Search Result 20090316\_112342\_us-10-552-515-2.rni.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10552515 and Search Result 20090316\_112342\_us-10-552-515-2.rni.

[Go Back to previous page](#)

GenCore version 6.3

Copyright (c) 1993 - 2009 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 16, 2009, 16:27:41 ; Search time 1151 Seconds  
(without alignments)  
20454.958 Million cell updates/sec

Title: US-10-552-515-2  
Perfect score: 3308  
Sequence: 1 aaaagatagatcctgctcca.....acctggtgaccttcgaatgt 3308

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9875436 seqs, 3558593875 residues

Total number of hits satisfying chosen parameters: 19750872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /ABSS/Data/CRF/ptodata/1/ina/1\_COMB.seq:\*  
2: /ABSS/Data/CRF/ptodata/1/ina/5\_COMB.seq:\*  
3: /ABSS/Data/CRF/ptodata/1/ina/6A\_COMB.seq:\*  
4: /ABSS/Data/CRF/ptodata/1/ina/6B\_COMB.seq:\*  
5: /ABSS/Data/CRF/ptodata/1/ina/7A\_COMB.seq:\*  
6: /ABSS/Data/CRF/ptodata/1/ina/7B\_COMB.seq:\*  
7: /ABSS/Data/CRF/ptodata/1/ina/7C\_COMB.seq:\*  
8: /ABSS/Data/CRF/ptodata/1/ina/7D\_COMB.seq:\*  
9: /ABSS/Data/CRF/ptodata/1/ina/HA\_COMB.seq:\*  
10: /ABSS/Data/CRF/ptodata/1/ina/HB\_COMB.seq:\*  
11: /ABSS/Data/CRF/ptodata/1/ina/PCTUS\_COMB.seq:\*  
12: /ABSS/Data/CRF/ptodata/1/ina/PP\_COMB.seq:\*  
13: /ABSS/Data/CRF/ptodata/1/ina/RE\_COMB.seq:\*  
14: /ABSS/Data/CRF/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	% Query						Description
	No.	Score	Match	Length	DB	ID	
	1	461	13.9	13243	6	US-10-741-601-5735	Sequence 5735, Ap
	2	461	13.9	13243	8	US-10-741-600-17879	Sequence 17879, A
	3	461	13.9	14172	6	US-10-741-601-5626	Sequence 5626, Ap
	4	461	13.9	14172	8	US-10-741-600-17603	Sequence 17603, A
c	5	460.6	13.9	101046	6	US-10-741-601-5689	Sequence 5689, Ap
c	6	460.6	13.9	101046	8	US-10-741-600-17753	Sequence 17753, A
	7	432.8	13.1	4509	8	US-10-912-745B-698	Sequence 698, App
	8	325.6	9.8	3052	5	US-10-342-887-1730	Sequence 1730, Ap
	9	301.6	9.1	3898	3	US-10-104-047-604	Sequence 604, App
	10	286.6	8.7	2736	3	US-10-104-047-571	Sequence 571, App
	11	252.6	7.6	2118	5	US-10-108-260A-2040	Sequence 2040, Ap
	12	239.2	7.2	2158	5	US-10-108-260A-1547	Sequence 1547, Ap
	13	216.2	6.5	1282	3	US-09-270-767-13982	Sequence 13982, A
	14	170.8	5.2	2293	3	US-10-104-047-1146	Sequence 1146, Ap
	15	157.2	4.8	2371	7	US-10-100-683-1599	Sequence 1599, Ap
	16	157.2	4.8	2371	7	US-11-001-793-1599	Sequence 1599, Ap
c	17	128.6	3.9	201	6	US-10-741-601-19564	Sequence 19564, A
c	18	128.6	3.9	201	8	US-10-741-600-53300	Sequence 53300, A
	19	125	3.8	969	3	US-09-188-930-11	Sequence 11, Appl
	20	125	3.8	969	3	US-09-312-283C-11	Sequence 11, Appl
	21	121.8	3.7	656	3	US-09-270-767-30062	Sequence 30062, A
	22	104	3.1	1803	3	US-09-774-528-294	Sequence 294, App
	23	104	3.1	1803	3	US-10-120-988-294	Sequence 294, App
	24	99.2	3.0	910	8	US-10-098-754-19306	Sequence 19306, A
	25	71.8	2.2	842	3	US-09-154-750A-72	Sequence 72, Appl
	26	70.2	2.1	571	3	US-09-270-767-187	Sequence 187, App
	27	70.2	2.1	571	3	US-09-270-767-15469	Sequence 15469, A
	28	70	2.1	201	8	US-10-741-600-64183	Sequence 64183, A
	29	66.6	2.0	394468	8	US-10-741-600-17952	Sequence 17952, A
	30	66	2.0	653	3	US-09-533-559-5580	Sequence 5580, Ap
	31	66	2.0	653	5	US-10-653-047-5580	Sequence 5580, Ap
c	32	65.4	2.0	11287	14	5523089-36	Patent No. 5523089
	33	64.6	2.0	11287	14	5523089-36	Patent No. 5523089
c	34	61	1.8	2846	7	US-09-815-264-90691	Sequence 90691, A
	35	60.8	1.8	201	6	US-10-741-601-23608	Sequence 23608, A
	36	60.8	1.8	201	8	US-10-741-600-64182	Sequence 64182, A
	37	58.2	1.8	7218	2	US-08-232-463-14	Sequence 14, Appl
	38	56.8	1.7	1926	3	US-09-249-585A-4	Sequence 4, Appli
	39	56.8	1.7	1931	2	US-09-130-114-2	Sequence 2, Appli
	40	56	1.7	1146	3	US-09-270-767-624	Sequence 624, App
	41	56	1.7	1146	3	US-09-270-767-15906	Sequence 15906, A
	42	55.6	1.7	3453	3	US-10-101-464A-861	Sequence 861, App
c	43	55.4	1.7	58408	7	US-09-815-264-81539	Sequence 81539, A
	44	55.2	1.7	125401	5	US-10-203-295-35	Sequence 35, Appl
	45	55	1.7	1320	3	US-09-902-540-8133	Sequence 8133, Ap

ALIGNMENTS

RESULT 1

US-10-741-601-5735  
; Sequence 5735, Application US/10741601  
; Patent No. 7306913  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001500  
; CURRENT APPLICATION NUMBER: US/10/741,601  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 26415  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5735  
; LENGTH: 13243  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(13243)  
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-2)  
US-10-741-601-5735

Query Match 13.9%; Score 461; DB 6; Length 13243;  
Best Local Similarity 100.0%; Pred. No. 1.5e-87;  
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2848	AGCTCAGCTCCCACTGGACACCCCTTCACGGTTCCCAAGGCCAGCCAGCTGCAGCAGTGAC	2907
Db	7463	AGCTCAGCTCCCACTGGACACCCCTTCACGGTTCCCAAGGCCAGCCAGCTGCAGCAGTGAC	7522
Qy	2908	GCCTGGAAGGACATCTGGTGGTCCTTAGGGGAGTGGCCCCTCCTGAGCCCTGCGAGCAGC	2967
Db	7523	GCCTGGAAGGACATCTGGTGGTCCTTAGGGGAGTGGCCCCTCCTGAGCCCTGCGAGCAGC	7582
Qy	2968	GTCCTTTTCTCTTCCCTCAGGCAGCGGCTGTGTGAACCGCTGGCTGCTGTTGTGCCTCA	3027
Db	7583	GTCCTTTTCTCTTCCCTCAGGCAGCGGCTGTGTGAACCGCTGGCTGCTGTTGTGCCTCA	7642
Qy	3028	TCTCTGGGCACATTGCCTGCTTCCCCCAGCGCCGGCTTCTCTCCTCAGAGCGCCTGTCA	3087
Db	7643	TCTCTGGGCACATTGCCTGCTTCCCCCAGCGCCGGCTTCTCTCCTCAGAGCGCCTGTCA	7702
Qy	3088	CTCCATCCCCGGCAGGGAGGGACCGTCAGCTCACAAGGCCCTCTTTGTTTCTGCTCCCA	3147
Db	7703	CTCCATCCCCGGCAGGGAGGGACCGTCAGCTCACAAGGCCCTCTTTGTTTCTGCTCCCA	7762
Qy	3148	GACATAAGCCCAAGGGGGCCCTGCACCCAAGGGACCCTGTCCCTCGGTGGCCTCCCCAGG	3207
Db	7763	GACATAAGCCCAAGGGGGCCCTGCACCCAAGGGACCCTGTCCCTCGGTGGCCTCCCCAGG	7822
Qy	3208	CCCCTGGACACGACAGTTCTCCTCAGGCAGGTGGGCTTTGTGGTCCTCGCCGCCCTGGC	3267

Db 7823 CCCCTGGACACGACAGTTCTCCTCAGGCAGGTGGGCTTTGTGGTCCTCGCCGCCCCTGGC 7882

Qy 3268 CACATCGCCCTCTCCTCTTACACCTGGTGACCTTCGAATGT 3308  
|||||

Db 7883 CACATCGCCCTCTCCTCTTACACCTGGTGACCTTCGAATGT 7923

RESULT 2

US-10-741-600-17879

; Sequence 17879, Application US/10741600

; Patent No. 7482117

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001499

; CURRENT APPLICATION NUMBER: US/10/741,600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 17879

; LENGTH: 13243

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(13243)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-2)

US-10-741-600-17879

Query Match 13.9%; Score 461; DB 8; Length 13243;

Best Local Similarity 100.0%; Pred. No. 1.5e-87;

Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2848 AGCTCAGCTCCCACTGGACACCCTTCACGGTTCCCAAGGCCAGCCAGCTGCAGCAGTGAC 2907  
|||||

Db 7463 AGCTCAGCTCCCACTGGACACCCTTCACGGTTCCCAAGGCCAGCCAGCTGCAGCAGTGAC 7522

Qy 2908 GCCTGGAAGGACATCTGGTGGTCCTTAGGGGAGTGGCCCCCTCTGAGCCCTGCGAGCAGC 2967  
|||||

Db 7523 GCCTGGAAGGACATCTGGTGGTCCTTAGGGGAGTGGCCCCCTCTGAGCCCTGCGAGCAGC 7582

Qy 2968 GTCCTTTTCTCTTCCCTCAGGCAGCGGCTGTGTGAACCGCTGGCTGCTGTTGTGCCTCA 3027  
|||||

Db 7583 GTCCTTTTCTCTTCCCTCAGGCAGCGGCTGTGTGAACCGCTGGCTGCTGTTGTGCCTCA 7642

Qy 3028 TCTCTGGGCACATTGCCTGCTTCCCCCAGCGCCGGCTTCTCTCCTCAGAGCGCCTGTCA 3087  
|||||

Db 7643 TCTCTGGGCACATTGCCTGCTTCCCCCAGCGCCGGCTTCTCTCCTCAGAGCGCCTGTCA 7702

Qy 3088 CTCCATCCCCGGCAGGGAGGGACCGTCAGCTCACAAGGCCCTCTTTGTTTCCTGCTCCCA 3147  
|||||

Db 7703 CTCCATCCCCGGCAGGGAGGGACCGTCAGCTCACAAGGCCCTCTTTGTTTCCTGCTCCCA 7762

Qy 3148 GACATAAGCCCAAGGGGCCCCTGCACCCAAGGGACCCTGTCCCTCGGTGGCCTCCCCAGG 3207  
|||||

```
Db      7763  GACATAAGCCCAAGGGGCCCCCTGCACCCAAGGGACCCTGTCCCTCGGTGGCCTCCCCAGG 7822

Qy      3208  CCCCTGGACACGACAGTTCTCCTCAGGCAGGTGGGCTTTGTGGTCCTCGCCGCCCTGGC 3267
        |||
Db      7823  CCCCTGGACACGACAGTTCTCCTCAGGCAGGTGGGCTTTGTGGTCCTCGCCGCCCTGGC 7882

Qy      3268  CACATCGCCCTCTCCTCTTACACCTGGTGACCTTCGAATGT 3308
        |||
Db      7883  CACATCGCCCTCTCCTCTTACACCTGGTGACCTTCGAATGT 7923
```

RESULT 3

US-10-741-601-5626

; Sequence 5626, Application US/10741601

; Patent No. 7306913

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001500

; CURRENT APPLICATION NUMBER: US/10/741,601

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 26415

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 5626

; LENGTH: 14172

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(14172)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-2)

US-10-741-601-5626

```
Query Match          13.9%;  Score 461;  DB 6;  Length 14172;
Best Local Similarity 100.0%;  Pred. No. 1.6e-87;
Matches 461;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

```
Qy      2848  AGCTCAGCTCCCACTGGACACCCCTTCACGGTTCCCAAGGCCAGCCAGCTGCAGCAGTGAC 2907
        |||
Db      2831  AGCTCAGCTCCCACTGGACACCCCTTCACGGTTCCCAAGGCCAGCCAGCTGCAGCAGTGAC 2890

Qy      2908  GCCTGGAAGGACATCTGGTGGTCCTTAGGGGAGTGGCCCCCTCCTGAGCCCTGCGAGCAGC 2967
        |||
Db      2891  GCCTGGAAGGACATCTGGTGGTCCTTAGGGGAGTGGCCCCCTCCTGAGCCCTGCGAGCAGC 2950

Qy      2968  GTCCTTTTCTCTTCCCTCAGGCAGCGGCTGTGTGAACCGCTGGCTGCTGTTGTGCCTCA 3027
        |||
Db      2951  GTCCTTTTCTCTTCCCTCAGGCAGCGGCTGTGTGAACCGCTGGCTGCTGTTGTGCCTCA 3010

Qy      3028  TCTCTGGGCACATTGCCTGCTTCCCCCAGCGCCGGCTTCTCTCCTCAGAGCGCCTGTCA 3087
        |||
Db      3011  TCTCTGGGCACATTGCCTGCTTCCCCCAGCGCCGGCTTCTCTCCTCAGAGCGCCTGTCA 3070

Qy      3088  CTCCATCCCCGGCAGGGAGGGACCGTCAGCTCACAAGGCCCTCTTTGTTTCCTGCTCCCA 3147
        |||
```

Db	3071	CTCCATCCCCGGCAGGGAGGGACCGTCAGCTCACAAGGCCCTCTTTGTTTCCTGCTCCCA	3130
Qy	3148	GACATAAGCCCAAGGGGCCCTGCACCCAAGGGACCCTGTCCCTCGGTGGCCTCCCCAGG	3207
Db	3131	GACATAAGCCCAAGGGGCCCTGCACCCAAGGGACCCTGTCCCTCGGTGGCCTCCCCAGG	3190
Qy	3208	CCCCTGGACACGACAGTTCTCCTCAGGCAGGTGGGCTTTGTGGTCCTCGCCGCCCTGGC	3267
Db	3191	CCCCTGGACACGACAGTTCTCCTCAGGCAGGTGGGCTTTGTGGTCCTCGCCGCCCTGGC	3250
Qy	3268	CACATCGCCCTCTCCTCTTACACCTGGTGACCTTCGAATGT	3308
Db	3251	CACATCGCCCTCTCCTCTTACACCTGGTGACCTTCGAATGT	3291

RESULT 4

US-10-741-600-17603

; Sequence 17603, Application US/10741600

; Patent No. 7482117

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001499

; CURRENT APPLICATION NUMBER: US/10/741,600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 17603

; LENGTH: 14172

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(14172)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-2)

US-10-741-600-17603

Query Match 13.9%; Score 461; DB 8; Length 14172;

Best Local Similarity 100.0%; Pred. No. 1.6e-87;

Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2848	AGCTCAGCTCCCCTGGACACCCCTTCACGGTTCCCAAGGCCAGCCAGCTGCAGCAGTGAC	2907
Db	2831	AGCTCAGCTCCCCTGGACACCCCTTCACGGTTCCCAAGGCCAGCCAGCTGCAGCAGTGAC	2890
Qy	2908	GCCTGGAAGGACATCTGGTGGTCCTTAGGGGAGTGGCCCCTCCTGAGCCCTGCGAGCAGC	2967
Db	2891	GCCTGGAAGGACATCTGGTGGTCCTTAGGGGAGTGGCCCCTCCTGAGCCCTGCGAGCAGC	2950
Qy	2968	GTCCTTTTCTCTTCCCTCAGGCAGCGGCTGTGTGAACCGCTGGCTGCTGTTGTGCCTCA	3027
Db	2951	GTCCTTTTCTCTTCCCTCAGGCAGCGGCTGTGTGAACCGCTGGCTGCTGTTGTGCCTCA	3010
Qy	3028	TCTCTGGGCACATTGCCTGCTTCCCCCAGCGCCGGCTTCTCTCCTCAGAGCGCCTGTCA	3087

```
Db      3011 TCTCTGGGCACATTGCCTGCTTCCCCCAGCGCCGGCTTCTCTCCTCAGAGCGCCTGTCA 3070
Qy      3088 CTCCATCCCCGGCAGGGAGGGACCGTCAGCTCACAAGGCCCTCTTTGTTTCCTGCTCCCA 3147
        |||
Db      3071 CTCCATCCCCGGCAGGGAGGGACCGTCAGCTCACAAGGCCCTCTTTGTTTCCTGCTCCCA 3130
Qy      3148 GACATAAGCCCAAGGGGCCCCCTGCACCCAAGGGACCCTGTCCCTCGGTGGCCTCCCCAGG 3207
        |||
Db      3131 GACATAAGCCCAAGGGGCCCCCTGCACCCAAGGGACCCTGTCCCTCGGTGGCCTCCCCAGG 3190
Qy      3208 CCCCTGGACACGACAGTTCTCCTCAGGCAGGTGGGCTTTGTGGTCCTCGCCGCCCTGGC 3267
        |||
Db      3191 CCCCTGGACACGACAGTTCTCCTCAGGCAGGTGGGCTTTGTGGTCCTCGCCGCCCTGGC 3250
Qy      3268 CACATCGCCCTCTCCTCTTACACCTGGTGACCTTCGAATGT 3308
        |||
Db      3251 CACATCGCCCTCTCCTCTTACACCTGGTGACCTTCGAATGT 3291
```

RESULT 5

US-10-741-601-5689/c

; Sequence 5689, Application US/10741601

; Patent No. 7306913

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001500

; CURRENT APPLICATION NUMBER: US/10/741,601

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 26415

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 5689

; LENGTH: 101046

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(101046)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-2)

US-10-741-601-5689

```
Query Match          13.9%;  Score 460.6;  DB 6;  Length 101046;
Best Local Similarity 99.8%;  Pred. No. 3.1e-87;
Matches 460;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;
```

```
Qy      2848 AGCTCAGCTCCCACTGGACACCCTTCACGGTTCCCAAGGCCAGCCAGCTGCAGCAGTGAC 2907
        |||
Db      97821 AGCTCAGCTCCCACTGGACACCCTTCACRGTTCCCAAGGCCAGCCAGCTGCAGCAGTGAC 97762
Qy      2908 GCCTGGAAGGACATCTGGTGGTCCTTAGGGGAGTGGCCCCCTCTGAGCCCTGCGAGCAGC 2967
        |||
Db      97761 GCCTGGAAGGACATCTGGTGGTCCTTAGGGGAGTGGCCCCCTCTGAGCCCTGCGAGCAGC 97702
Qy      2968 GTCCTTTTCTCTTCCCTCAGGCAGCGGCTGTGTGAACCGCTGGCTGCTGTTGTGCCTCA 3027
        |||
```

Db	97701	GTCCTTTTCTCTTCCCTCAGGCAGCGGCTGTGTGAACCGCTGGCTGCTGTTGTGCCTCA	97642
Qy	3028	TCTCTGGGCACATTGCCTGCTTCCCCCAGCGCCGGCTTCTCTCCTCAGAGCGCCTGTCA	3087
Db	97641	TCTCTGGGCACATTGCCTGCTTCCCCCAGCGCCGGCTTCTCTCCTCAGAGCGCCTGTCA	97582
Qy	3088	CTCCATCCCCGGCAGGGAGGGACCGTCAGCTCACAAGGCCCTCTTTGTTTCCTGCTCCCA	3147
Db	97581	CTCCATCCCCGGCAGGGAGGGACCGTCAGCTCACAAGGCCCTCTTTGTTTCCTGCTCCCA	97522
Qy	3148	GACATAAGCCCAAGGGGCCCTGCACCCAAGGGACCCTGTCCCTCGGTGGCCTCCCCAGG	3207
Db	97521	GACATAAGCCCAAGGGGCCCTGCACCCAAGGGACCCTGTCCCTCGGTGGCCTCCCCAGG	97462
Qy	3208	CCCCTGGACACGACAGTTCTCCTCAGGCAGGTGGGCTTTGTGGTCCTCGCCGCCCTGGC	3267
Db	97461	CCCCTGGACACGACAGTTCTCCTCAGGCAGGTGGGCTTTGTGGTCCTCGCCGCCCTGGC	97402
Qy	3268	CACATCGCCCTCTCCTCTTACACCTGGTGACCTTCGAATGT	3308
Db	97401	CACATCGCCCTCTCCTCTTACACCTGGTGACCTTCGAATGT	97361

RESULT 6

US-10-741-600-17753/c

; Sequence 17753, Application US/10741600

; Patent No. 7482117

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001499

; CURRENT APPLICATION NUMBER: US/10/741,600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 17753

; LENGTH: 101046

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(101046)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-2)

US-10-741-600-17753

Query Match 13.9%; Score 460.6; DB 8; Length 101046;

Best Local Similarity 99.8%; Pred. No. 3.1e-87;

Matches 460; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	2848	AGCTCAGCTCCCCTGGACACCCCTTCACGGTTCCCAAGGCCAGCCAGCTGCAGCAGTGAC	2907
Db	97821	AGCTCAGCTCCCCTGGACACCCCTTCACRGTTCCCAAGGCCAGCCAGCTGCAGCAGTGAC	97762
Qy	2908	GCCTGGAAGGACATCTGGTGGTCCTTAGGGGAGTGGCCCCCTCTGAGCCCTGCGAGCAGC	2967



Db	97761	GCCTGGAAGGACATCTGGTGGTCCTTAGGGGAGTGGCCCCCTCTGAGCCCTGCGAGCAGC	97702
Qy	2968	GTCCTTTTCTCTTCCCTCAGGCAGCGGCTGTGTGAACCGCTGGCTGCTGTTGTGCCTCA	3027
Db	97701	GTCCTTTTCTCTTCCCTCAGGCAGCGGCTGTGTGAACCGCTGGCTGCTGTTGTGCCTCA	97642
Qy	3028	TCTCTGGGCACATTGCCTGCTTCCCCCAGCGCCGGCTTCTCTCCTCAGAGCGCCTGTCA	3087
Db	97641	TCTCTGGGCACATTGCCTGCTTCCCCCAGCGCCGGCTTCTCTCCTCAGAGCGCCTGTCA	97582
Qy	3088	CTCCATCCCCGGCAGGGAGGGACCGTCAGCTCACAAGGCCCTCTTTGTTTCCTGCTCCCA	3147
Db	97581	CTCCATCCCCGGCAGGGAGGGACCGTCAGCTCACAAGGCCCTCTTTGTTTCCTGCTCCCA	97522
Qy	3148	GACATAAGCCCAAGGGGGCCCCTGCACCCAAGGGACCCTGTCCCTCGGTGGCCTCCCCAGG	3207
Db	97521	GACATAAGCCCAAGGGGGCCCCTGCACCCAAGGGACCCTGTCCCTCGGTGGCCTCCCCAGG	97462
Qy	3208	CCCCTGGACACGACAGTTCTCCTCAGGCAGGTGGGCTTTGTGGTCCTCGCCGCCCTGGC	3267
Db	97461	CCCCTGGACACGACAGTTCTCCTCAGGCAGGTGGGCTTTGTGGTCCTCGCCGCCCTGGC	97402
Qy	3268	CACATCGCCCTCTCCTCTTACACCTGGTGACCTTCGAATGT	3308
Db	97401	CACATCGCCCTCTCCTCTTACACCTGGTGACCTTCGAATGT	97361

RESULT 7

US-10-912-745B-698

; Sequence 698, Application US/10912745B

; Patent No. 7473531

; GENERAL INFORMATION

; APPLICANT: DOMON, Bruno et al.

; TITLE OF INVENTION: Pancreatic Cancer Targets and Uses

; TITLE OF INVENTION:Thereof

; FILE REFERENCE: CL001538

; CURRENT APPLICATION NUMBER: US/10/912,745B

; CURRENT FILING DATE: 2004-08-06

; NUMBER OF SEQ ID NOS: 875

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 698

; LENGTH: 4509

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-912-745B-698

Query Match 13.1%; Score 432.8; DB 8; Length 4509;  
Best Local Similarity 55.5%; Pred. No. 1.2e-81;  
Matches 977; Conservative 0; Mismatches 747; Indels 36; Gaps 6;

Qy	841	AGGACACCTTCTTCACAAGCACCAAGAGGCACCAAATTCTGTTTGAGATCCTGGCCAAGA	900
Db	875	AGGATTCTCTTTTCGACAGCAAAACCCGGAGCACGATTGTCTATGAGATCTTGAAGAGAA	934
Qy	901	CCCCGTATGGCCACGAGAAGAAAAACCTGCTTGGGATCCACCAGCTGCTGGCAGAGGGTG	960

Db	935	CGACGTGTACAAAGGCCAAGTACAGCATG---GGCATCACGAGCCTGCTGGCCAATGGTG	991
Qy	961	TCCTCAGTGCCGCCCTTCCCCCTGCATGACGGCCCCCTTCAAGACGCCCCCAGAGGGCCCCG	1020
Db	992	TGTACGCGGCTGCATACCCACTGCACGATGGAGACTACAACGGTGAAAACGTCGAGT---	1048
Qy	1021	AGGCTCCACGCCTCAACCAGCGCCAAGTCCTTTTCCAGCACTGGGCGCGCTGGGGCAAGT	1080
Db	1049	-----TCAACGACAGAAACTCCTGTACGAAGAGTGGGCACGCTATGGAGTTT	1096
Qy	1081	GGAACAAGTACCAGCCCCTGGACCACGTGCGCAGGTACTTCGGGGAGAAGGTGGCCCTCT	1140
Db	1097	TCTATAAGTACCAGCCCATCGACCTGGTCAGGAAGTATTTTGGGGAGAAGATCGGCCTGT	1156
Qy	1141	ACTTCGCCTGGCTCGGGTTTTACACAGGCTGGCTCCTGCCAGCGGCAGTGGTGGGCACAC	1200
Db	1157	ACTTCGCCTGGCTGGGCGTGTACACCCAGATGCTCATCCCTGCCTCCATCGTGGGAATCA	1216
Qy	1201	TGGTGTTCCTGGTGGGCTGCTTCCTGGTGTTCCTCAGACATACCCACGCAGGAAGTGTGTG	1260
Db	1217	TTGTCTTCCTGTACGGATGCGCCACCATGGATGAAAACATCCCCAGCATGGAGATGTGTG	1276
Qy	1261	GCAGCAAGGACAGCTTCGAGATGTGCCACTTTGCCTCGA--CTGCCCTTTCTGGCTGC	1317
Db	1277	ACCAGAGACACAATATCACCATGTGCCCGCTTTGCGACAAGACCTGCAGCTACTGGAAGA	1336
Qy	1318	TCTCCAGCGCCTGTGCCCTGGCCCAGGCCGGCGGCTGTTTCGACCACGGCGGCACCGTGT	1377
Db	1337	TGAGCTCAGCCTGCGCCACGGCCCGCGCCAGCCACCTCTTCGACAACCCCGCCACGGTCT	1396
Qy	1378	TCTTCAGCTTGTTTCATGGCACTGTGGGCCGTGCTGCTGCTGGAGTACTGGAAGCGGAAGA	1437
Db	1397	TCTTCTCTGTCTTCATGGCCCTCTGGGCTGCCACCTTCATGGAGCACTGGAAGCGGAAAC	1456
Qy	1438	GCGCCACGCTGGCCTACCGCTGGGACTGCTCTGACTACGAGGACACTGAGGAGAGGCCTC	1497
Db	1457	AGATGCGACTCAACTACCGCTGGGACCTCACGGGCTTTGAAGAGGAAGAGGATCATCCTA	1516
Qy	1498	GGCCCCAGTTTGCCGCTCAGCCCCCATGACAGCCCCGAA-----CCCCATCACGG	1548
Db	1517	GAGCTGAATACGAAGCCAGAGTCTTGAGAAGTCTCTGAAGAAAGAGTCCAGAAACAAAG	1576
Qy	1549	GTGAGGACGAGCCCTACTTCCCTGAGAGGAGCCGCGCGCGCCGCATGCTGGCCGGCTCTG	1608
Db	1577	AGACTGACAAAGTGAAGCTGACATGGAGAGATCGGTTCCCAGCCTACCTACTAAGTGG	1636
Qy	1609	TGGTGATCGTGGTGATGGTGGCCGTGGTGGTCATGTGCCTCGTGTCTATCATCCTGTACC	1668
Db	1637	TCTCCATCATCTTCATGATTGCAGTGACGTTTGCCATCGTCCTCGGCGTCATCATCTACA	1696
Qy	1669	GTGCCATCATGGCCATCGTGGTGTCCAGGTCGGGCAACACCCTTCTCGCAGCCTGGGCCT	1728
Db	1697	GAATCTCCATGGCCGCGCCTTGGCCATGAACTCCTCCCCCTCCGTGCGGTCCAACATCC	1756
Qy	1729	CTCGCATGCCAGCCTCACGGGGTCTGTAGTGAACCTCGTCTTCATCCTCATCCTCTCCA	1788

Db	1757	GGGTCACAGTCACAGCCACCGCAGTCATCATCAACCTAGTGGTCATCATCCTCCTGGACG	1816
Qy	1789	AGATCTATGTATCCCTGGCCCACGTCCTGACACGATGGGAAATGCACCGCACCCAGACCA	1848
Db	1817	AGGTGTATGGCTGCATAGCCCGATGGCTCACCAAGATCGAGGTCCCAAAGACGGAGAAAA	1876
Qy	1849	AGTTCGAGGACGCCTTCACCCTCAAGGTGTTTCATCTTCCAGTTCGTCAACTTCTACTCCT	1908
Db	1877	GCTTTGAGGAGAGGCTGATCTTCAAGGCTTTCCTGCTGAAGTTTGTGAATTCCTACACCC	1936
Qy	1909	CACCCGTCTACATTGCCTTCTTCAAGGGCAGGTTTGTGGGATACCCAGGCAACTAC---C	1965
Db	1937	CCATCTTTTACGTGGCGTTCTTCAAAGGCCGTTTGTGACGCCCGGGCGACTACGTGT	1996
Qy	1966	ACACCTTGTTTGGAGTCCGCAATGAGGAGTGC GCGGCTGGAGGCTGCCTGATCGAGCTGG	2025
Db	1997	ACATTTTCCGTTCTTCCGAATGGAAGAGTGTGCGCCAGGGGGCTGCCTGATGGAGCTAT	2056
Qy	2026	CACAGGAGCTCCTGGTCATCATGGTGGGCAAGCAGGTCATC---AACAAACATGCAGGAGG	2082
Db	2057	GCATCCAGCTCAGCATCATCATGCTGGGGAAACAGCTGATCCAGAACAACCTGTTTCGAGA	2116
Qy	2083	TCCTCATCCCGAAGCTAAAGGGCTGGTGGCAGAAGTTCCGGCTTCGCTCCAAGAAGAGGA	2142
Db	2117	TCGGCATCCCGAAGATGAAGAAGCTCATCCGCTACCTGAAGCTGAAGCAGCAGAGCCCCC	2176
Qy	2143	AGGCGGGAGCTTCTGCAGGGGCTAGCCAGGGGCCCTGGGAGGACGACTATGAGCTTGTGC	2202
Db	2177	CTGACCACGAGGAGTGTGTGAAGAGGAAACAGCGGTACGAGGTGGATTACAACCTGGAGC	2236
Qy	2203	CCTGTGAGGGTCTGTTTGACGAGTACCTGGAAATGGTGTGTCAGTTCCGGCTTCGTACCA	2262
Db	2237	CCTTCGCGGGCCTCACCCCAGAGTACATGGAATGATCATCCAGTTTGGCTTCGTACCC	2296
Qy	2263	TCTTCGTGGCCGCCTGTCCGCTCGCGCCGCTCTTCGCCCTGCTCAACAACTGGGTGGAGA	2322
Db	2297	TGTTTGTGCGCTCCTTCCCCCTGGCCCCACTGTTTGCCTGCTGAACAACATCATCGAGA	2356
Qy	2323	TCCGCTTGACGCGCGCAAGTTTCGTCTGCGAGTACCGGCGCCCTGTGGCCGAGCGCGCCC	2382
Db	2357	TCCGCCTGGACGCCAAAAAGTTTGTCACTGAGCTCCGAAGGCCGGTAGCTGTCAGAGCCA	2416
Qy	2383	AGGACATCGGCATCTGGTTCCACATCCTGGCGGGCCTCACGCACCTGGCGGTCATCAGCA	2442
Db	2417	AAGACATCGGAATCTGGTACAATATCCTCAGAGGCATTGGGAAGCTTGCTGTCATCATCA	2476
Qy	2443	ACGCCTTCCTCCTGGCCTTCTCGTCCGACTTCCTGCCGCGCGCCTACTACCGGTGGACCC	2502
Db	2477	ATGCCTTCGTGATCTCCTTCACGTCTGACTTCATCCCGCGCCTGGTGTACCTCTACATGT	2536
Qy	2503	GCGCCACGACCTGCGCGGCTTCCTCAACTTCACGCTGGCGCGAGCCCCGTCCTCCTTCG	2562
Db	2537	ACAGTAAGAACGGGACCATGCACGGCTTCGTCAACCACACCCTCTCCTCCTTCAACGTCA	2596
Qy	2563	CCGCCGCGCACAACCGCACG	2582

Db 2597 GTGACTTCCAGAACGGCACG 2616

RESULT 8

US-10-342-887-1730  
; Sequence 1730, Application US/10342887  
; Patent No. 7171311  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Christopher J.  
; APPLICANT: Van 't Veer, Laura Johanna  
; APPLICANT: Van de Vijver, Marc J.  
; APPLICANT: Bernards, Rene  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
; FILE REFERENCE: 9301-188-999  
; CURRENT APPLICATION NUMBER: US/10/342,887  
; CURRENT FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: 60/298,918  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/380,710  
; PRIOR FILING DATE: 2002-05-14  
; PRIOR APPLICATION NUMBER: 10/172,118  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 2699  
; SEQ ID NO 1730  
; LENGTH: 3052  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-342-887-1730

Query Match 9.8%; Score 325.6; DB 5; Length 3052;  
Best Local Similarity 55.1%; Pred. No. 6e-59;  
Matches 759; Conservative 0; Mismatches 589; Indels 30; Gaps 5;

Qy	1235	AGACATACCCACGCAGGA	ACTGTGTGGCAGCAAGGACAGCTTCGAGATGTGCCC	ACTTTG	1294
Db	7	AAACATCCCAGCATGGAGATGTGTGACCAGAGACACAATATCACCATGTGCCCGCTTTG	66		
Qy	1295	CCTCGA---	CTGCCCTTTCTGGCTGCTCTCCAGCGCCTGTGCCCTGGCCCAGGCCG	CGCCG	1351
Db	67	CGACAAGACCTGCAGCTACTGGAAGATGAGCTCAGCCTGCGCCACGGCCCGCGCCAGCCA	126		
Qy	1352	GCTGTTCGACCACGGCGGCACCGTGTTC	TTCAGCTTGTTTCATGGCACTGTGGG	CCGTGCT	1411
Db	127	CCTCTTCGACAACCCCGCCACGGTCTTCTTCTCTGTCTTCATGGCCCTCTGGGCTGCCAC	186		
Qy	1412	GCTGCTGGAGTACTGGAAGCGGAAGAGCGCCACGCTGGCCTACCGCTGGGACTGCTCTGA	1471		
Db	187	CTTCATGGAGCACTGGAAGCGGAAACAGATGCGACTCAACTACCGCTGGGACCTCACGGG	246		
Qy	1472	CTACGAGGACACTGAGGAG-----	AGGCCTCGGCCCCAGTTTGCCGCCTCAGC	1519	
Db	247	CTTTGAAGAGGAAGAGGAGGCTGTCAAGGATCATCCTAGAGCTGAATACGAAGCCAGAGT	306		

Qy	1520	CCCCATGACAGCCCCGAACCCCATCACGGGTGAGGACGAGCCCTACTTCCCTGAGAGGAG	1579
Db	307	CTTGGAGAAGTCTCTGAAGAAAGAGTCCAGAAACAAAGAGACTGACAAAGTGAAGCTGAC	366
Qy	1580	CCGCGCGCGCCGCATGCTGGCCGG-----CTCTGTGGTGATCGTGGTGATGGTGGC	1630
Db	367	ATGGAGAGATCGGTTCCAGCCTACCTCACTAACTTGGTCTCCATCATCTTCATGATTGC	426
Qy	1631	CGTGGTGGTCATGTGCCTCGTGTCTATCATCTGTACCGTGCCATCATGGCCATCGTGGT	1690
Db	427	AGTGACGTTTGCCATCGTCCTCGGCGTCATCATCTACAGGATCTCCATGGCCGCCGCTT	486
Qy	1691	GTCCAGGTCGGGCAACACCCTTCTCGCAGCCTGGGCCTCTCGCATCGCCAGCCTCACGGG	1750
Db	487	GGCCATGAACCTCCTCCCCCTCCGTGCGGTCCAACATCCGGGTACAGTCACAGCCACCGC	546
Qy	1751	GTCTGTAGTGAACCTCGTCTTCATCCTCATCCTCTCCAAGATCTATGTATCCCTGGCCCA	1810
Db	547	GGTCATCATCAACCTAGTGGTCATCATCCTCCTGGACGAGGTGTATGGCTGCATAGCCCG	606
Qy	1811	CGTCCTGACACGATGGGAAATGCACCGCACCCAGACCAAGTTCGAGGACGCCTTCACCCT	1870
Db	607	ATGGCTCACCAAGATCGAGGTCCCAAAGACGGAGAAAAGCTTTGAGGAGAGGCTGATCTT	666
Qy	1871	CAAGGTGTTTCATCTTCCAGTTCGTCAACTTCTACTCCTCACCCGTCTACATTGCCTTCTT	1930
Db	667	CAAGGCTTTCCTGCTGAAGTTTGTGAATTCCTACACCCCATCTTTTACGTGGCGTTCTT	726
Qy	1931	CAAGGGCAGGTTTGTGGGATACCCAGGCAACTACC---ACACCTTGTTTGGAGTCCGCAA	1987
Db	727	CAAAGGCCGGTTTGTGGACGCCCCGGGCGACTACGTGTACATTTTCCGTTCTTCCGAAT	786
Qy	1988	TGAGGAGTGC GCGGCTGGAGGCTGCCTGATCGAGCTGGCACAGGAGCTCCTGGTCATCAT	2047
Db	787	GGAAGAGTGTGCGCCAGGGGCTGCCTGATGGAGCTATGCATCCAGCTCAGCATCATCAT	846
Qy	2048	GGTGGGCAAGCAGGTCATC---AACACATGCAGGAGTCTCATCCCGAAGCTAAAGGG	2104
Db	847	GCTGGGGAAACAGCTGATCCAGAACAACCTGTTTCGAGATCGGCATCCCGAAGATGAAGAA	906
Qy	2105	CTGGTGGCAGAAGTTCCGGCTTCGCTCCAAGAAGAGGAAGGCGGGAGCTTCTGCAGGGGC	2164
Db	907	GCTCATCCGCTACCTGAAGCTGAAGCAGCAGAGCCCCCTGACCACGAGGAGTGTGTGAA	966
Qy	2165	TAGCCAGGGGCCCTGGGAGGACGACTATGAGCTTGTGCCCTGTGAGGGTCTGTTTGACGA	2224
Db	967	GAGGAAACAGCGGTACGAGGTGGATTACAACCTGGAGCCCTTCGCGGGCCTCACCCAGA	1026
Qy	2225	GTACCTGGAAATGGTGTGCAGTTCGGCTTCGTACCATCTTCGTGGCCGCCTGTCCGCT	2284
Db	1027	GTACATGGAAATGATCATCCAGTTTGGCTTCGTACCCCTGTTTGTGCGCTCCTTCCCCCT	1086
Qy	2285	CGCGCCGCTCTTCGCCCTGCTCAACAACCTGGGTGGAGATCCGCTTGGACGCGCGCAAGTT	2344
Db	1087	GGCCCCACTGTTTGCCTGCTGAACAACATCATCGAGATCCGCCTGGACGCCAAAAGTT	1146

Qy	2345	CGTCTGCGAGTACCGGCGCCCTGTGGCCGAGCGCGCCCAGGACATCGGCATCTGGTTCCA	2404
Db	1147	TGTCCTGAGCTCCGAAGGCCGGTAGCTGTCAGAGCCAAAGACATCGGAATCTGGTACAA	1206
Qy	2405	CATCCTGGCGGGCCTCACGCACCTGGCGGTCATCAGCAACGCCTTCCTCCTGGCCTTCTC	2464
Db	1207	TATCCTCAGAGGCATTGGGAAGCTTGCTGTCATCATCAATGCCTTCGTGATCTCCTTCAC	1266
Qy	2465	GTCCGACTTCCTGCCGCGCGCCTACTACCGGTGGACCCGCGCCACGACCTGCGCGGCTT	2524
Db	1267	GTCTGACTTCATCCCGCGCCTGGTGTACCTCTACATGTACAGTAAGAACGGGACCATGCA	1326
Qy	2525	CCTCAACTTCACGCTGGCGCGAGCCCCGTCCTCCTTCGCCGCCGCGCACAACCGCACG	2582
Db	1327	CGGCTTCGTCAACCACACCCTCTCCTCCTTCAACGTCAGTGACTTCCAGAACGGGCACG	1384

RESULT 9

US-10-104-047-604  
; Sequence 604, Application US/10104047  
; Patent No. 6943241  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. 6943241e1 full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 604  
; LENGTH: 3898  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-104-047-604

Query Match 9.1%; Score 301.6; DB 3; Length 3898;			
Best Local Similarity 50.9%; Pred. No. 8e-54;			
Matches 871; Conservative 0; Mismatches 824; Indels 15; Gaps 6;			
Qy	780	GAGTACTACTCCTGCCGTTTCTCAGAGTGAACAAGCTGCCACGCTTCCTCGGGAGTGACAAC	839
Db	950	GACTGCTACACTGCCCCTTTCAGCCAGCAAAGGATCCATCACTTCATC---ATACACAAC	1006
Qy	840	CAGGACACCTTCTTCACAAGCACCAAGAGGCACCAAATTCTGTTTGAGATCCTGGCCAAG	899
Db	1007	AAAGAAACGTTCTTCAACAATGCCACAAGAAGTAGAATCGTGCATCACATTTTACAAAGA	1066
Qy	900	ACCCCGTATGGCCACGAGAAGAAAAACCTGCTTGGGATCCACCAGCTGCTGGCAGAGGGT	959
Db	1067	ATAAAATATG---AAGAAGGAAAAACAAGATTGGTCTGAATCGTTTGCTTACCAATGGC	1123
Qy	960	GTCCTCAGTGCCGCCTTCCCCCTGCATGACGGCCCCCTTCAAGACGCCCCCAGAGGGCCCG	1019

Db	1124	TCCTATGAAGCTGCGTTTCCCCTGCATGAGGGAAGTTATAGAAGTAAAACTCCATTCTGA	1183
Qy	1020	CAGGCTCCACGCCTCAACCAGCGCCAAGTCCTTTTCCAGCACTGGGCGCGCTGGGGCAAG	1079
Db	1184	ACCCATGGAGCAGAAAACCACCGACATCTACTCTATGAGTGCTGGGCCTCCTGGGGCGTG	1243
Qy	1080	TGGAACAAGTACCAGCCCCTGGACCACGTGCGCAGGTACTTCGGGGAGAAGGTGGCCCTC	1139
Db	1244	TGGTATAAATACCAACCTTTGGATCTTGTAAGGCGGTACTTTGGAGAGAAGATTGGGTTA	1303
Qy	1140	TACTTCGCCTGGCTCGGGTTTTACACAGGCTGGCTCCTGCCAGCGGCAGTGGTGGGCACA	1199
Db	1304	TATTTTGCCTGGTTGGGCTGGTACACCGGCATGCTCTTCCCAGCTGCCTTCATTGGATTG	1363
Qy	1200	CTGGTGTTCCTGGTGGGCTGCTTCCTGGTGTTCAGACATAACCCACGCAGGAAGTGTGT	1259
Db	1364	TTTGTCTTTTTGTATGGCGTCACCACTCTGGATCACAGCCAAGTCAGTAAAGAAGTCTGC	1423
Qy	1260	GGCAGCAAGGACAGCTTCGAGATGTGCCCACTTTGCCTCGACTGCCCTTCTGGCTGCTC	1319
Db	1424	CAAGCTACAGATATCATCATGTGTCTGTGTGATAAATACTGTCCATTCATGAGGCTG	1483
Qy	1320	TCCAGCGCCTGTGCCCTGGCCCAGGCCGCGCGCTGTTCGACCACGGCGGCACCGTGTTC	1379
Db	1484	TCAGACAGCTGTGTATATGCCAAGGTAACCCACCTTTTGGACAATGGAGCCACTGTCTTC	1543
Qy	1380	TTCAGCTTGTTTCATGGCACTGTGGGCGGTGCTGCTGCTGGAGTACTGGAAGCGGAAGAGC	1439
Db	1544	TTTGCTGTTTTTCATGGCAGTCTGGGCAACAGTTTTCTGGAGTTTTGGAAAAGACGGCGA	1603
Qy	1440	GCCACGCTGGCCTACCGCTGGGACTGCTCTGACTACGAGGACACTGAGGAGAGGCCTCGG	1499
Db	1604	GCAGTAATTGCTTATGACTGGGATTTGATAGACTGGGAAGAAGAGGAGGAAGAAATACGA	1663
Qy	1500	CCCCAGTTTGCCGCCTCAGCCCCCATGACAGCCC---CGAACCCCATCACGGGTGAGGAC	1556
Db	1664	CCCCAGTTTGAAGCCAAGTATTCCAAGAAAGAGCGGATGAATCCAATTTCTGGAAAGCCA	1723
Qy	1557	GAGCCCTACTTCCCTGAGAGGAGCCGCGCGCGCCGCATGCTGGCCGGCTCTGTGGTGATC	1616
Db	1724	GAACCTTATCAAGCATTTACAGATAAATGCAGCAGACTTATCGTTTCTGCATCTGGAATA	1783
Qy	1617	GTGGTGATGGTGGCCGTGGTGGTCATGTGCCTCGTGTCTATCATCCTGTACCGTGCCATC	1676
Db	1784	TTTTTTATGATCTGCGTGGTGATTGCTGCCGTGTTTCGGGATCGTCATTTACCGGGTGGTG	1843
Qy	1677	ATGGCCATCGTGGTGTCCAGGTCGGGCAACACCCTTCTCGCAGCCTGGGCCTCTCGCATC	1736
Db	1844	ACTGTCAGCACTTTCGCTGCCTTTAAGTGGGCGTTAATCAGGAATAACTCTCAGGTTGCA	1903
Qy	1737	GCCAGCCTCACGGGGTCTGTAGTGAACCTCGTCTTCATCCTCATCCTCTCCAAGATCTAT	1796
Db	1904	ACCACAGGGACTGCTGTGTGCATCAACTTCTGTATCATTATGTTGCTGAATGTGCTCTAT	1963
Qy	1797	GTATCCCTGGCCCACGTCCTGACACGATGGGAAATGCACCGCACCCAGACCAAGTTCGAG	1856

Db	1964	GAAAAAGTTGCCCTGCTTCTGACGAATTTAGAACAGCCTCGCACAGAGTCTGAGTGGGAG	2023
Qy	1857	GACGCCTTCACCCTCAAGGTGTTTCATCTTCCAGTTTCGTCAACTTCTACTCCTCACCCGTC	1916
Db	2024	AACAGCTTCACCCTGAAAATGTTTCTTTTTCAGTTTGTCAATCTGAACAGCTCCACATTT	2083
Qy	1917	TACATTGCCTTCTTCAAGGGCAGGTTTGTGGGATACCCAGGCAACTACCACACCTTGTT-	1975
Db	2084	TACATCGCATTCTTCCTCGGAAGATTTACAGGACACCCAGGTGCCTACTTGAGGCTGATA	2143
Qy	1976	--TGGAGTCCGCAATGAGGAGTGC GCGGCTGGAGGCTGCCTGATCGAGCTGGCACAGGAG	2033
Db	2144	AACAGGTGGAGACTAGAAGAGTGCCACCCTAGTGATGCCTTATTGATCTGTGTATGCAA	2203
Qy	2034	CTCCTGGTCATCATGGTGGGCAAGCAGGTCATCAACAACATGCAGGAGGTCCCTCATCCCG	2093
Db	2204	ATGGGTATTATAATGGTGCTAAAGCAGACCTGGAATAATTTTCATGGAACCTGGCTACCCG	2263
Qy	2094	AAGCTAAAGGGCTGGTGGCAGAAGTTCCGGCTTCGCTCCAAGAAGAGGAAGGCGGGAGCT	2153
Db	2264	TTAATTCAGAATTGGTGGACTAGAAGAAAAGTACG--ACAAGAACATGGACCTGAAAGGA	2321
Qy	2154	TCTGCAGGGGCTAGCCAGGGGCCCTGGGAGGACGACTATGAGCTTGTGCCCTGTGAGGGT	2213
Db	2322	AAATAAGTTTCCCACAATGGGAAA-AGGACTATAACCTTCAGCCGATGAATGCCTATGGA	2380
Qy	2214	CTGTTTGACGAGTACCTGGAAATGGTGTGCGAGTTCGGCTTCGTCACCATCTTCGTGGCC	2273
Db	2381	CTCTTCGATGAATACTTAGAAATGATTCTTCAGTTTGGATTCACAACTATCTTTGTGGCA	2440
Qy	2274	GCCTGTCCGCTCGCGCCGCTCTTCGCCCTGCTCAACAACCTGGGTGGAGATCCGCTTGAC	2333
Db	2441	GCTTTTCCCTAGCACCCTTCTGGCCTTACTGAATAACATAATTGAAATTCGACTTGAT	2500
Qy	2334	GCGCGCAAGTTCGTCTGCGAGTACCGGCGCCCTGTGGCCGAGCGCGCCCAGGACATCGGC	2393
Db	2501	GCTTACAAATTTGTCACACAGTGGAGGAGACCTTTAGCTTCAAGGGCCAAAGACATAGGA	2560
Qy	2394	ATCTGGTTCCACATCCTGGCGGGCCTCACGCACCTGGCGGTCATCAGCAACGCCCTTCCTC	2453
Db	2561	ATTTGGTATGGAATTCTTGAAGGCATTGGAATTCTCTCTGTTATCACAAATGCATTTGTC	2620
Qy	2454	CTGGCCTTCTCGTCCGACTTCCTGCCGCGC	2483
Db	2621	ATAGCGATAACATCTGACTTTATCCCTCGC	2650

RESULT 10

US-10-104-047-571

; Sequence 571, Application US/10104047

; Patent No. 6943241

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: No. 6943241e1 full length cDNA

; FILE REFERENCE: H1-A0105

; CURRENT APPLICATION NUMBER: US/10/104,047



; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 571  
; LENGTH: 2736  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-104-047-571

Query Match 8.7%; Score 286.6; DB 3; Length 2736;  
Best Local Similarity 51.7%; Pred. No. 1.1e-50;  
Matches 752; Conservative 0; Mismatches 694; Indels 9; Gaps 4;

Qy	1035	AACCAGCGCCAAGTCCTTTTCCAGCACTGGGCGCGCTGGGGCAAGTGGAACAAGTACCAG	1094
Db	31	AACCACCGACATCTACTCTATGAGTGCTGGGCCTCCTGGGGCGTGTGGTATAAATACCAA	90
Qy	1095	CCCCTGGACCACGTGCGCAGGTACTTCGGGGAGAAGGTGGCCCTCTACTTCGCCTGGCTC	1154
Db	91	CCTTTGGATCTTGTAAAGGCGGTACTTTGGAGAGAAGATTGGGTTATATTTTGCCTGGTTG	150
Qy	1155	GGTTTTACACAGGCTGGCTCCTGCCAGCGGCAGTGGTGGGCACACTGGTGTTCTGGTG	1214
Db	151	GGCTGGTACACCGGCATGCTCTTCCCAGCTGCCTTCATTGGATTGTTTGTCTTTTGTAT	210
Qy	1215	GGCTGCTTCCTGGTGTTCTCAGACATACCCACGCAGGAAGTGTGTGGCAGCAAGGACAGC	1274
Db	211	GGCGTCACCACTCTGGATCACAGCCAAGTCAGTAAAGAAGTCTGCCAAGCTACAGATATC	270
Qy	1275	TTCGAGATGTGCCCCACTTTGCCTCGACTGCCCTTTCTGGCTGCTCTCCAGCGCCTGTGCC	1334
Db	271	ATCATGTGTCTGTGTGTGATAAATACTGTCCATTCATGAGGCTGTCAGACAGCTGTGTA	330
Qy	1335	CTGGCCCAGGCCGGCCGGCTGTTTCGACCACGGCGGCACCGTGTTCTTCAGCTTGTTTCATG	1394
Db	331	TATGCCAAGGTAACCCACCTTTTTGACAATGGAGCCACTGTCTTCTTTGCTGTTTTCATG	390
Qy	1395	GCACTGTGGGCCGTGCTGCTGCTGGAGTACTGGAAGCGGAAGAGCGCCACGCTGGCCTAC	1454
Db	391	GCAGTCTGGGCAACAGTTTTCTGGAGTTTTTGAAAAGACGGCGAGCAGTAATTGCTTAT	450
Qy	1455	CGCTGGGACTGCTCTGACTACGAGGACACTGAGGAGAGGCCTCGGCCCCAGTTTGCCGCC	1514
Db	451	GACTGGGATTTGATAGACTGGGAAGAAGAGGAGGAAGAAATACGACCCCAGTTTGAAGCC	510
Qy	1515	TCAGCCCCCATGACAGCCCC---GAACCCCATCACGGGTGAGGACGAGCCCTACTTCCCT	1571
Db	511	AAGTATTCCAAGAAAGAGCGGATGAATCCAATTTCTGGAAAGCCAGAACCTTATCAAGCA	570
Qy	1572	GAGAGGAGCCGCGCGCGCCGCATGCTGGCCGGCTCTGTGGTGATCGTGGTGATGGTGGCC	1631
Db	571	TTTACAGATAAATGCAGCAGACTTATCGTTTCTGCATCTGGAATATTTTTTATGATCTGC	630
Qy	1632	GTGGTGGTCATGTGCCTCGTGTCTATCATCCTGTACCGTGCCATCATGGCCATCGTGGTG	1691

Db	631	GTGGTGATTGCTGCCGTGTTTCGGGATCGTCATTTACCGGGTGGTGACTGTCAGCACTTTC	690
Qy	1692	TCCAGGTCGGGCAACACCCCTTCTCGCAGCCTGGGCCCTCTCGCATCGCCAGCCTCACGGGG	1751
Db	691	GCTGCCTTTAAGTGGGCGTTAATCAGGAATAACTCTCAGGTTGCAACCACAGGGACTGCT	750
Qy	1752	TCTGTAGTGAACCTCGTCTTCATCCTCATCCTCTCCAAGATCTATGTATCCCTGGCCCAC	1811
Db	751	GTGTGCATCAACTTCTGTATCATTATGTTGCTGAATGTGCTCTATGAAAAAGTTGCCCTG	810
Qy	1812	GTCCTGACACGATGGGAAATGCACCGCACCCAGACCAAGTTCGAGGACGCCTTCACCCTC	1871
Db	811	CTTCTGACGAATTTAGAACAGCCTCGCACAGAGTCTGAGTGGGAGAACAGCTTCACCCTG	870
Qy	1872	AAGGTGTTTCATCTTCCAGTTTCGTCAACTTCTACTCCTCACCCGTCTACATTGCCTTCTTC	1931
Db	871	AAAATGTTTCTTTTTCAGTTTGTCAATCTGAACAGCTCCACATTTTACATCGCATTCTTC	930
Qy	1932	AAGGGCAGGTTTGTGGGATACCCAGGCAACTACCACACCTTGTT---TGGAGTCCGCAAT	1988
Db	931	CTCGGAAGATTTACAGGACACCCAGGTGCCTACTTGAGGCTGATAAACAGGTGGAGACTA	990
Qy	1989	GAGGAGTGC GCGGCTGGAGGCTGCCTGATCGAGCTGGCACAGGAGCTCCTGGTCATCATG	2048
Db	991	GAAGAGTGCCACCCTAGTGGATGCCTTATTGATCTGTGTATGCAAATGGGTATTATAATG	1050
Qy	2049	GTGGGCAAGCAGGTCATCAACAACATGCAGGAGGTCCTCATCCGAAGCTAAAGGGCTGG	2108
Db	1051	GTGCTAAAGCAGACCTGGAATAATTTTCATGGAACCTGGCTACCCGTTAATTCAGAATTGG	1110
Qy	2109	TGGCAGAAGTTCCGGCTTCGCTCCAAGAAGAGGAAGGCGGGAGCTTCTGCAGGGGCTAGC	2168
Db	1111	TGGACTAGAAGAAAAGTACG--ACAAGAACATGGACCTGAAAGGAAAATAAGTTTCCCAC	1168
Qy	2169	CAGGGGCCCTGGGAGGACGACTATGAGCTTGTGCCCTGTGAGGGTCTGTTTGACGAGTAC	2228
Db	1169	AATGGG-AAAAGGACTATAACCTTCAGCCGATGAATGCCTATGGACTCTTCGATGAATAC	1227
Qy	2229	CTGGAATGGTGCTGCAGTTTCGGCTTCGTCACCATCTTCGTGGCCGCCTGTCCGCTCGCG	2288
Db	1228	TTAGAAATGATTCTTCAGTTTGGATTACAACTATCTTTGTGGCAGCTTTTCCCCTAGCA	1287
Qy	2289	CCGCTCTTCGCCCTGCTCAACAACCTGGGTGGAGATCCGCTTGGACGCGCGCAAGTTCGTC	2348
Db	1288	CCACTTCTGGCCTTACTGAATAACATAATTGAAATTCGACTTGATGCTTACAAATTTGTC	1347
Qy	2349	TGCGAGTACCGGCGCCCTGTGGCCGAGCGCGCCCAGGACATCGGCATCTGGTTCCACATC	2408
Db	1348	ACACAGTGAGGAGACCTTTAGCTTCAAGGGCCAAAGACATAGGAATTTGGTATGGAATT	1407
Qy	2409	CTGGCGGGCCTCACGCACCTGGCGGTCATCAGCAACGCCTTCCTCCTGGCCTTCTCGTCC	2468
Db	1408	CTTGAAGGCATTGGAATTCTCTCTGTTATCACAAATGCATTTGTCATAGCGATAACATCT	1467
Qy	2469	GACTTCCTGCCGCGC	2483

||||| | || |||  
Db 1468 GACTTTATCCCTCGC 1482

RESULT 11

US-10-108-260A-2040

; Sequence 2040, Application US/10108260A

; Patent No. 7193069

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: No. 7193069e1 full length cDNA

; FILE REFERENCE: H1-A0106

; CURRENT APPLICATION NUMBER: US/10/108,260A

; CURRENT FILING DATE: 2002-03-27

; NUMBER OF SEQ ID NOS: 5458

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2040

; LENGTH: 2118

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-108-260A-2040

Query Match 7.6%; Score 252.6; DB 5; Length 2118;  
Best Local Similarity 54.3%; Pred. No. 1.7e-43;  
Matches 616; Conservative 0; Mismatches 489; Indels 30; Gaps 4;

Qy	841	AGGACACCTTCTTCACAAGCACCAAGAGGCACCAAATTCTGTTTGAGATCCTGGCCAAGA	900
Db	731	AGGATTCTTTTTTCGACAGCAAAACCCGGAGCACGATTGTCTATGAGATCTTGAAGAGAA	790
Qy	901	CCCCGTATGGCCACGAGAAGAAAAACCTGCTTGGGATCCACCAGCTGCTGGCAGAGGGTG	960
Db	791	CGACGTGTACAAAGGCCAAGTACAGCATG---GGCATCACGAGCCTGCTGGCCAATGGTG	847
Qy	961	TCCTCAGTGCCGCCTTCCCCCTGCATGACGGCCCCCTCAAGACGCCCCCAGAGGGCCCGC	1020
Db	848	TGTACGCGGCTGCATACCCACTGCACGATGGAGACTACAACGGTGAAAACGTCGAGT---	904
Qy	1021	AGGCTCCACGCCTCAACCAGCGCCAAGTCCTTTTCCAGCACTGGGCGCGCTGGGGCAAGT	1080
Db	905	-----TCAACGACAGAAACTCCTGTACGAAGAGTGGGCACGCTATGGAGTTT	952
Qy	1081	GGAACAAGTACCAGCCCCTGGACCACGTGCGCAGGTACTTCGGGGAGAAGGTGGCCCTCT	1140
Db	953	TCTATAAGTACCAGCCCATCGACCTGGTCAGGAAGTATTTTGGGGAGAAGATCGGCCTGT	1012
Qy	1141	ACTTCGCCTGGCTCGGGTTTTACACAGGCTGGCTCCTGCCAGCGGCAGTGGTGGGCACAC	1200
Db	1013	ACTTCGCCTGGCTGGGCGTGTACACCCAGATGCTCATCCCTGCCTCCATCGTGGGAATCA	1072
Qy	1201	TGGTGTTCCTGGTGGGCTGCTTCCTGGTGTTCCTCAGACATACCCACGCAGGAAGTGTGTG	1260
Db	1073	TTGTCTTCCTGTACGGATGCGCCACCATGGATGAAAACATCCCCAGCATGGAGATGTGTG	1132
Qy	1261	GCAGCAAGGACAGCTTCGAGATGTGCCCACTTTGCCTCGA---CTGCCCTTTCTGGCTGC	1317

Db	1133	ACCAGAGACACAATATCACCATGTGCCCGCTTTGCGACAAGACCTGCAGCTACTGGAAGA	1192
Qy	1318	TCTCCAGCGCCTGTGCCCTGGCCCAGGCCGCGCGGCTGTTTCGACCACGGCGGCACCGTGT	1377
Db	1193	TGAGCTCAGCCTGCGCCACGGCCCGCGCCAGCCACCTCTTCGACAACCCCGCCACGGTCT	1252
Qy	1378	TCTTCAGCTTGTTTCATGGCACTGTGGGCCGTGCTGCTGCTGGAGTACTGGAAGCGGAAGA	1437
Db	1253	TCTTCTCTGTCTTCATGGCCCTCTGGGCTGCCACCTTCATGGAGCACTGGAAGCGGAAAC	1312
Qy	1438	GCGCCACGCTGGCCTACCGCTGGGACTGCTCTGACTACGAGGACACTGAGGAGAGGCCTC	1497
Db	1313	AGATGCGACTCAACTACCGCTGGGACCTCACGGGCTTTGAAGAGGAAGAGGATCATCCTA	1372
Qy	1498	GGCCCCAGTTTGCCGCCTCAGCCCCCATGACAGCCCCGAACCCCATCACGGGTGAGGACG	1557
Db	1373	GAGCTGAATACGAAGCCAGAGTCTTGAGAAAGTCTCTGAAGAAAGAGTCCAGAAACAAAG	1432
Qy	1558	AGCCCTACTTCCCTGAGAGGAGCCGCGCGCGCCGCATGCTGGCC-----GGCTCTG	1608
Db	1433	AGACTGACAAAGTGAAGCTGACATGGAGAGATCGGTTCCCAGCCTACCTACTAACTTGG	1492
Qy	1609	TGGTGATCGTGGTGATGGTGGCCGTGGTGGTCATGTGCCTCGTGTCTATCATCCTGTACC	1668
Db	1493	TCTCCATCATCTTCATGATTGCAGTGACGTTTGCCATCGTCCTCGGCGTCATCATCTACA	1552
Qy	1669	GTGCCATCATGGCCATCGTGGTGTCCAGGTCGGGCAACACCCTTCTCGCAGCCTGGGCCT	1728
Db	1553	GGATCTCCATGGCCGCCGCCTTGGCCATGAACTCCTCCCCCTCCGTGCGGTCCAACATCC	1612
Qy	1729	CTCGCATCGCCAGCCTCACGGGGTCTGTAGTGAACCTCGTCTTCATCCTCATCCTCTCCA	1788
Db	1613	GGGTCACAGTCACAGCCACCGCGGTCATCATCAACCTAGTGGTCATCATCCTCCTGGACG	1672
Qy	1789	AGATCTATGTATCCCTGGCCCACGTCCTGACACGATGGGAAATGCACCGCACCCAGACCA	1848
Db	1673	AGGTGTATGGCTGCATAGCCCGATGGCTCACCAAGATCGAGGTCCCAAAGACGGAGAAAA	1732
Qy	1849	AGTTCGAGGACGCCCTTACCCTCAAGGTGTTTCATCTTCCAGTTCGTCAACTTCTACTCCT	1908
Db	1733	GCTTTGAGGAGAGGCTGATCTTCAAGGCTTTCCTGCTGAAGTTTGTGAATTCCTACACCC	1792
Qy	1909	CACCCGTCTACATTGCCTTCTTCAAGGGCAGGTTTGTGGGATACCCAGGCAACTA	1963
Db	1793	CCATCTTTTACGTGGCGTTCTTCAAAGGCCGGTTTGTGACGCCCGGGCGACTA	1847

RESULT 12

US-10-108-260A-1547

; Sequence 1547, Application US/10108260A

; Patent No. 7193069

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: No. 7193069e1 full length cDNA

; FILE REFERENCE: H1-A0106

; CURRENT APPLICATION NUMBER: US/10/108,260A

; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1547  
; LENGTH: 2158  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-260A-1547

Query Match 7.2%; Score 239.2; DB 5; Length 2158;  
Best Local Similarity 52.3%; Pred. No. 1.2e-40;  
Matches 693; Conservative 0; Mismatches 568; Indels 63; Gaps 5;

Qy	1508	TGCCGCCTCAGCCCCCATGACAGCCCCGAACCCCATCACGGGTGAGGACGAGCCCTACTT	1567
Db	276	TGCCGTGTCTGAGGAGGAAATGGCACTTCAGCTCATTAAGTCCCCGACTACAAGCTCCG	335
Qy	1568	CCCTGAGAGGAGCCGCGCGCGCCGCATGCTGGCCGGCTCTGTGGTGATCGTGGTGATGGT	1627
Db	336	GCCATACCAGCACTCCTACCTACGCAGCACCCTCATCCTCGTCCTGACCCTGCTCATGAT	395
Qy	1628	GGCCGTGGTGGTCATGTGCCTCGTGTCTATCATCCTGTACCGTGCCATCATGGCCATCGT	1687
Db	396	CTGCCTCATGATCGGCATGGCCCACGTCCTGGTGGTCTACCGCGTCCTGGCCTCCGCGCT	455
Qy	1688	GGTGTCCAGGTCGGGCAACACCCTTCTCGCAGCCTGGGCCTCTCGCATCGCCAGCCTCAC	1747
Db	456	CTTCAGCAGCTCGGCCGTGCCCTTCCTGGAGGAGCAGGTGACCACGGCCGTGGTGGTGAC	515
Qy	1748	GGGGTCTGTAGTGAACCTCGTCTTCATCCTCATCCTCTCCAAGATCTATGTATCCCTGGC	1807
Db	516	CGGGGCTCTGGTGCACATATGTGACCATCGTCATCATGACCAAGATCAACAGGCGCGTGGC	575
Qy	1808	CCACGTCCTGACACGATGGGAAATGCACCGCACCCAGACCAAGTTCGAGGACGCCTTCAC	1867
Db	576	CCTGAAGCTTTGTGACTTCGAGATGCCCAGGACCTTCTCGGAGCGAGAGAGCAGGTTTAC	635
Qy	1868	CCTCAAGGTGTTTCATCTTCCAGTTTCGTCAACTTCTACTCCTCACCCGTCTACATTGCCTT	1927
Db	636	CATCCGCTTCTTCACACTGCAGTTCTTCACCATTTCTCGTCTCTCATCTACATCGCCTT	695
Qy	1928	CTTCAAGGGCAGGTTTGTGGGATACCCAGGCAACTACCACACCTTGTTTGGAGTCCGCAA	1987
Db	696	CATCCTGGGCAGGATCAACGGCCACCCGGGAAGTCCACGCGCCTGGCGGGCTTGTGGAA	755
Qy	1988	---TGAGGAGTGCGCGGCTGGAGGCTGCCTGATCGAGCTGGCACAGGAGCTCCTGGTCAT	2044
Db	756	GCTGGAAGAGTGCCACGCCAGCGGCTGCATGATGGACCTCTTCGTGCAGATGGCCATCAT	815
Qy	2045	CATGGTGGGCAAGCAGGTCATCAACAACATGCAGGAGGTCCTCATCCCGAAGCTAAAGGG	2104
Db	816	CATGGGCCTGAAGCAGACGCTCAGCAACTGCGTCGAGTACCTGGTCCCGTGGGTGACCCA	875
Qy	2105	CTGGTGGCAGAAAGTTCCGGCTTCGCTCCAAGAAGAGGAAGGCGGGAGCTTCTGCAGGGGC	2164
Db	876	CAAGTGCC---GCTCTCTGCGGGCTCCGAGTCCGGGCACCTGCCCCGGGACCCCGAGCT	932

Qy	2165	TAGCCAGGGGCCCTGGGAGGACGACTATGAGCTTGTGCCCTGTGAGGGTCTGTTTGACGA	2224
Db	933	CAGGGACTGGCGGCGCAACTACCTTCTGAACCCGGTCAACACCTTCAGCCTGTTTCGACGA	992
Qy	2225	GTACCTGGAAATGGTGTGTCAGTTCGGCTTCGTACCATCTTCGTGGCCGCCTGTCCGCT	2284
Db	993	GTTTCATGGAGATGATGATCCAGTACGGCTTCACCACCATCTTCGTGGCCGCCTTCCCGCT	1052
Qy	2285	CGCGCCGCTCTTCGCCCTGCTCAACAACTGGGTGGAGATCCGCTTGGACGCGCGCAAGTT	2344
Db	1053	GGCGCCGCTGCTCGCGCTCTTCAGCAACCTCGTGGAGATCCGCCTGGACGCCATCAAGAT	1112
Qy	2345	CGTCTGCGAGTACCGGCGCCCTGTGGCCGAGCGCGCCCAGGACATCGGCATCTGGTTCCA	2404
Db	1113	GGTCTGGTTGCAGCGGCGCCTGGTGCCGCGCAAGGCCAAGGACATCGGGACCTGGCTGCA	1172
Qy	2405	CATCCTGGCGGGCCTCACGCACCTGGCGGTCATCAGCAACGCCTTCCTCCTGGCCTTCTC	2464
Db	1173	GGTGCTGGAGACCATCGGTGTGCTGGCGGTCATTGCCAATGGGATGGTCATTGCCTTCAC	1232
Qy	2465	GTCCGACTTCCTGCCGCGCGCCTACTACCGGTGGACCCGCGCCACGACCTG-----	2516
Db	1233	ATCTGAGTTCATCCCCCGAGTGGTCTACAAGTACCGCTATAGCCCATGCCTGAAAGAAGG	1292
Qy	2517	-----CGCGGCTTCCTCAACTTCACGCTGGCGCGAGCCCCGTCTCCTTCGCCGC	2566
Db	1293	CAACTCTACTGTCTGACTGCCTCAAGGGCTACGTCAACCACAGCCTGTCCGTCTTCCACAC	1352
Qy	2567	CGCGCACAACC-----GCACGTGCAGGTA	2590
Db	1353	CAAGGACTTCCAGGACCCTGATGGGATTGAGGGCTCAGAAAACGTGACTCTGTGCAGATA	1412
Qy	2591	TCGGGCTTTCCGGGAT---GACGATGGACATTATTCCCAGACCTACTGGAATCTTCTTGC	2647
Db	1413	CAGGGACTACCGCAATCCCCCGATTACAACCTTCTCCGAGCAGTTCTGGTTCCTCCTGGC	1472
Qy	2648	CATCCGCCTGGCCTTCGTTCATTGTGTTTGAGCATGTGGTTTTCTCCGTTGGCCGCCTCCT	2707
Db	1473	CATCCGCCTGGCCTTCGTTCATCTCTTTGAGCACGTGGCCTTGTGCATCAAGCTCATCGC	1532
Qy	2708	GGACCTCCTGGTGCCTGACATCCCAGAGTCTGTGGAGATCAAAGTGAAGCGGGAGTACTA	2767
Db	1533	CGCCTGGTTTCGTGCCCAGACATCCCTCAGTCGGTGAAGAACAAGTTCTGGAGGTGAAGTA	1592
Qy	2768	CCTG 2771	
Db	1593	CCAG 1596	

RESULT 13

US-09-270-767-13982

; Sequence 13982, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13982  
; LENGTH: 1282  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-13982

Query Match 6.5%; Score 216.2; DB 3; Length 1282;  
Best Local Similarity 53.9%; Pred. No. 8.2e-36;  
Matches 496; Conservative 0; Mismatches 413; Indels 12; Gaps 2;

Qy	1587	CGCCGCATGCTGGCCGGCTCTGTGGTGATCGTGGTGATGGTGGCCGTGGTGGTCATGTGC	1646
Db	169	CCCGCCACCGTGTTTCAGCTTTTCAGTGGTACTGCTCCTAATTGCACTGGCCTTTGTGGCA	228
Qy	1647	CTCGTGTCTATCATCCTGTACCGTGCCATCATGGCCATCGTGGTGTCCAGGTCGGGCAAC	1706
Db	229	CTGCTGGCAGTGTTGTATACCGAATGTCCATGCTGGCCGCCCTTAAAGTGGGTGCTAGT	288
Qy	1707	ACCCTTCTCGCAGCCTGGGCCTCTCGCATCGCCAGCCTCACGGGTCTGTAGTGAACCTC	1766
Db	289	CCCATGACCACCTCTAGCGCTATTGTCCTAGCCACTGCATCAGCTGCCTTTGTAAATCTG	348
Qy	1767	GTCTTCATCCTCATCCTCTCCAAGATCTATGTATCCCTGGCCCACGTCCTGACACGATGG	1826
Db	349	TGCCTGCTCTATATACTTAATTATATGTACAATCATTTGGCTGAGTACCTGACAGAGCTG	408
Qy	1827	GAAATGCACCGCACCCAGACCAAGTTCGAGGACGCCTTCACCCTCAAGGTGTTTCATCTTC	1886
Db	409	GAAATGTGGCGCACTCAAACCTCAGTTCGATGACTCGCTTACCCTTAAATTTATCTGCTG	468
Qy	1887	CAGTTCGTCAACTTCTACTCCTCACCCGTCTACATTGCCTTCTTCAAGGGCAGGTTTGTG	1946
Db	469	CAGTTTGTAAACTACTACGCCTCCATTTTTTACATAGCTTTCTTCAAGGGTAAATTCGTT	528
Qy	1947	GGATACCCAGGCAACTACCACACCTTGTTTGGAGTCCGCAATGAGGAGTGC GCGGCTGGA	2006
Db	529	GGTCATCCGGGAGAGTATAATAAGCTTTTTGACTATCGGCAGGAGGAGTGCTCATCGGGT	588
Qy	2007	GGCTGCCTGATCGAGCTGGCACAGGAGCTCCTGGTCATCATGGTGGGCAAGCAGGTCATC	2066
Db	589	GGCTGTTTAAACGGAGCTGTGCATCCAGTTAGCCATTATAATGGTTGGCAAGCAGGCATTC	648
Qy	2067	AACAACATGCAGGAGG-----TCCTCATCCCGAAGCTAAAGGGCTGGTGGCAGAAGTTC	2120
Db	649	AACACTATTCTTGAAGTGTATCTTCCCATGTTCTGGCGAAAGGTTTTGGCCATTCAGGTG	708
Qy	2121	CGGCTTCGCTCCAAGAAGAGGAAGGCGGGAGCTTCTGCAGGGGCTAGCCAGGGGCCCTGG	2180
Db	709	GGCCTGTCGCGACTTTTCAACAACACCCCGAATCCAGACAAGACGAAAGACGAACGCTGG	768

Qy	2181	GAGGACGACTATGAGCTTGTGCCCTGTGAG-----GGTCTGTTTGACGAGTACCTGGAA	2234
Db	769	ATGCGGGATTTC AAGCTACTGGATTGGGGTGCCCGAGGTCTGTTTCCCGAGTATTGGAG	828
Qy	2235	ATGGTGCTGCAGTTCGGCTTCGTACCATCTTCGTGGCCGCCTGTCCGCTCGCGCCGCTC	2294
Db	829	ATGGTCTTGCAGTACGGCTTCGTAACCATCTTTGTGGCCGCTTTTCCGCTGGCGCCATTC	888
Qy	2295	TTCGCCCTGCTCAACAACCTGGGTGGAGATCCGCTTGGACGCGCGCAAGTTCGTCTGCGAG	2354
Db	889	TTTGCCCTGCTAAATAATATCTTGAAATGCGACTGGATGCAAAGAAACTATTGACCCAC	948
Qy	2355	TACCGGCGCCCTGTGGCCGAGCGCGCCCAGGACATCGGCATCTGGTTCCACATCCTGGCG	2414
Db	949	CACAAGCGTCCAGTATCACAGCGAGTTCGAGATATAGGAGTGTGGTATCGTATCCTGGAC	1008
Qy	2415	GGCCTCACGCACCTGGCGGTCATCAGCAACGCCTTCCTCCTGGCCTTCTCGTCCGACTTC	2474
Db	1009	TGCATAGGCAAGCTCAGCGTGATCAAAATGGATTTCATCATAGCCTTTACCTCTGACATG	1068
Qy	2475	CTGCCGCGCGCCTACTACCGG	2495
Db	1069	ATTCCGCGTTTGGTGTACCGG	1089

RESULT 14

US-10-104-047-1146  
; Sequence 1146, Application US/10104047  
; Patent No. 6943241  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. 6943241e1 full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1146  
; LENGTH: 2293  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-104-047-1146

Query Match	5.2%;	Score 170.8;	DB 3;	Length 2293;
Best Local Similarity	54.9%;	Pred. No. 4.1e-26;		
Matches	400;	Conservative	0;	Mismatches 322; Indels 6; Gaps 3;
Qy	1759	TGAACCTCGTCTTCATCCTCATCCTCTCCAAGATCTATGTATCCCTGGCCCACGTCCTGA	1818	
Db	324	TCAACTTCTGTATCATTATGTTGCTGAATGTGCTCTATGAAAAAGTTGCCCTGCTTCTGA	383	
Qy	1819	CACGATGGGAAATGCACCGCACCCAGACCAAGTTCGAGGACGCCTTCACCCTCAAGGTGT	1878	
Db	384	CGAATTTAGAACAGCCTCGCACAGAGTCTGAGTGGGAGAACAGCTTCACCCTGAAAATGT	443	



Qy	1879	TCATCTTCCAGTTCGTCAACTTCTACTCCTCACCCGTCTACATTGCCTTCTTCAAGGGCA	1938
Db	444	TTCTTTTTTCAGTTTGTCAATCTGAACAGCTCCACATTTTACATCGCATTCTTCCTCGGAA	503
Qy	1939	GGTTTGTGGGATACCCAGGCAACTACCACACCTTGTT---TGGAGTCCGCAATGAGGAGT	1995
Db	504	GATTTACAGGACACCCAGGTGCCTACTTGAGGCTGATAAACAGGTGGAGACTAGAAGAGT	563
Qy	1996	GCGCGGCTGGAGGCTGCCTGATCGAGCTGGCACAGGAGCTCCTGGTCATCATGGTGGGCA	2055
Db	564	GCCACCCTAGTGGATGCCTTATTGATCTGTGTATGCAAATGGGTATTATAATGGTGCTAA	623
Qy	2056	AGCAGGTCATCAACAACATGCAGGAGGTCTCATCCCGAAGCTAAAGGGCTGGTGGCAGA	2115
Db	624	AGCAGACCTGGAATAATTTTCATGGAACCTGGCTACCCGTTAATTCAGAATTGGTGGACTA	683
Qy	2116	AGTTCCGGCTTCGCTCCAAGAAGAGGAAGGCGGGAGCTTCTGCAGGGGCTAGCCAGGGGC	2175
Db	684	GAAGAAAAGTACG--ACAAGAACATGGACCTGAAAGGAAAATAAGTTTCCCACAATGGG-	740
Qy	2176	CCTGGGAGGACGACTATGAGCTTGTGCCCTGTGAGGGTCTGTTTGACGAGTACCTGGAAA	2235
Db	741	AAAAGGACTATAACCTTCAGCCGATGAATGCCTATGGACTCTTCGATGAATACTTAGAAA	800
Qy	2236	TGGTGTGTCAGTTTCGGCTTCGTCACCATCTTCGTGGCCGCCTGTCCGCTCGCGCCGCTCT	2295
Db	801	TGATTCTTCAGTTTGGATTCACAACTATCTTTGTGGCAGCTTTTCCCCTAGCACCCTTC	860
Qy	2296	TCGCCCTGCTCAACAACCTGGGTGGAGATCCGCTTGGACGCGCGCAAGTTCGTCTGCGAGT	2355
Db	861	TGGCCTTACTGAATAACATAATTGAAATTCGACTTGATGCTTACAAATTTGTCACACAGT	920
Qy	2356	ACCGGCGCCCTGTGGCCGAGCGCGCCCAGGACATCGGCATCTGGTTCCACATCCTGGCGG	2415
Db	921	GGAGGAGACCTTTAGCTTCAAGGGCCAAAGACATAGGAATTTGGTATGGAATTCTTGAAG	980
Qy	2416	GCCTCACGCACCTGGCGGTATCAGCAACGCCTTCCTCCTGGCCTTCTCGTCCGACTTCC	2475
Db	981	GCATTGGAATTCTCTCTGTTATCACAAATGCATTTGTCATAGCGATAACATCTGACTTTA	1040
Qy	2476	TGCCGCGC	2483
Db	1041	TCCCTCGC	1048

RESULT 15

US-10-100-683-1599

; Sequence 1599, Application US/10100683

; Patent No. 7368531

; GENERAL INFORMATION:

; APPLICANT: Rosen, et al.

; TITLE OF INVENTION: Human Secreted Proteins

; FILE REFERENCE: PS900

; CURRENT APPLICATION NUMBER: US/10/100,683

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: US 60/040,162  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: US 60/043,576  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: US 60/047,601  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: US 60/056,845  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: US 60/043,580  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: US 60/047,599  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: US 60/056,664  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: US 60/043,314  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: US 60/047,632  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: US 60/056,892  
; PRIOR FILING DATE: 1997-08-22  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 13468  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1599  
; LENGTH: 2371  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-100-683-1599

Query Match 4.8%; Score 157.2; DB 7; Length 2371;  
Best Local Similarity 61.9%; Pred. No. 3.2e-23;  
Matches 249; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

Qy	2181	GAGGACGACTATGAGCTTGTGCCCTGTGAGGGTCTGTTTGACGAGTACCTGGAAATGGTG	2240
Db	6	GAGGTGGATTACAACCTGGAGCCCTTCGCGGGCCTCACCCCAGAGTACATGGAAATGATC	65
Qy	2241	CTGCAGTTCGGCTTCGTCACCATCTTCGTGGCCGCTGTCCGCTCGCGCCGCTCTTCGCC	2300
Db	66	ATCCAGTTTGCTTCGTCACCCTGTTTGTGCGCTCCTTCCCCCTGGCCCCACTGTTTGCG	125
Qy	2301	CTGCTCAACAACCTGGGTGGAGATCCGCTTGGACGCGCGCAAGTTCGTCTGCGAGTACCGG	2360
Db	126	CTGCTGAACAACATCATCGAGATCCGCCTGGACGCCAAAAGTTTGTCACTGAGCTCCGA	185
Qy	2361	CGCCCTGTGGCCGAGCGCGCCAGGACATCGGCATCTGGTTCCACATCCTGGCGGGCCTC	2420
Db	186	AGGCCGGTAGCTGTGAGAGCCAAAGACATCGGAATCTGGTACAATATCCTCAGAGGCATT	245
Qy	2421	ACGCACCTGGCGGTCATCAGCAACGCCTTCCTCCTGGCCTTCTCGTCCGACTTCCTGCCG	2480
Db	246	GGGAAGCTTGCTGTGTCATCATCAATGCCTTCGTGATCTCCTTCACGTCTGACTTCATCCCG	305
Qy	2481	CGCGCTACTACCGGTGGACCCGCGCCACGACCTGCGCGGCTTCCTCAACTTCACGCTG	2540
Db	306	CGCCTGGTGTACCTCTACATGTACAGTAAGAACGGGACCATGCACGGCTTCGTCAACCAC	365

Qy	2541	GCGCGAGCCCCGTCCTCCTTCGCCGCCGCGCACAACCGCACG	2582
Db	366	ACCCTCTCCTCCTTCAACGTCAGTGACTTCCAGAACGGCACG	407

Search completed: March 16, 2009, 16:47:17  
Job time : 1176 secs

SCORE 2.0